

TTTMRTHSGERPYRCSCKR3FSDSSTLTKHLRIHSGERPYOCKLCLLRFSSQGNLNR
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1104 5481

5482.5612
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exon

intron
/gene="g1"
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intron
/gene="gl"
-1,000:EPGN0004618

exon
/gene="g1"
EB00004618"

BASE COUNT	2857 a	2220 c	2220 d
ORIGIN			

Query Match	84.0%	Score 16.8;	DB 33;	Length 9954;	
Best Local Similarity	90.0%	Pred. No. 42;			
Matches	18;	Mismatches	2;	Indels	0;
		Conservative		Gaps	0;

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Ox      1  ctgggcttactgtctatccg  20
          | | | | | | | | | | | |
Db      7129 cctgggcttAGTCTATCCG  7148

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RESULT 6
AC014473/c
AC014473 81901 bp DNA HTG 16-NOV-1999
*** SEQUENCING IN PROGRESS *** In ordered

LOCUS: MT010110
 SPECIES: *Prosochilia melanogaster*,
 pieces.
 ACCESSION: J0014473
 VERSION: J0014473.1 GI:6436862
 KEYWORDS: HTGS_PHASE2.
 SOURCE: fruit fly.
 ORGANISM: *Prosochilia melanogaster*
 Drosophila melanogaster
 Insecta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
 Metazoa; Dittena; Brachycera;

REFERENCE

1 (bases 1 to 1000) Adams, M. and Venter, J.C.

<p> AUTHORS TITLE JOURNAL COMMENT </p>	<p> Direct Submission Submitted (15-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, usa This sequence was identified as CDN:10211864 by the submitter. For further information on this sequence e-mail to flycelera.com or further information on this sequence. </p>
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* NOTE: This is a temporary
* This sequence will be replaced
* by the finished sequence as soon as it
* the accession number will be preserved

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FEATURES
source
1. .81901
/organism="Drosophila melanogaster"

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BASE COUNT	ORIGIN
22813 a	17895 c 18040 g

	Matches	18: Conservative	0: Mismatches	2: Indels	0: Gaps	0:
QY	1	cttggcgttaactctatcgcg	20			
Db	36832	CTGGGACCTTAAGTCAATCCG	36813			

RESULT	7	HTG	03-SEP-1999
AC007890			RP1-96
AC007890	121256 bp	DNA	
LOCUS		Chromosome 3	clone BACR02621 (D72)
DEFINITION			*** SEQUENCING IN PROGRESS
	02.6-21 map	905-91a	strain Y: cn bw sp, **

ACCESSION AC007890.4 GI:5828637
VERSION AC007890.4
KEYWORDS HTG; HTGS_PMSSEL.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Taxonomy Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Diptera; Diptera; Ecdysozoa; Ecdysozoa; Diptera; Dipterygota;

[illegible]

Doyle, C.M., Farfan, D.B., Gaele, S.R., Kaira, K., Reaney, R.A., Houston, K.A., Hummasti, S.R., Lomanta, M.A., Mazda, P., Hoskins, R.A., Lewis, S., Li, P., Lomanta, M.A., Park, S., Kim, E., Lee, B., Lewis, M., Nixon, K., Peckol, J.M., Park, S., Koshel, A.R., Koshel, M., Nixon, K., Peckol, J.M., Sait, E., Koshel, A.R., Koshel, M., Nixon, K., Peckol, J.M., Sait, E., Peiffer, B., Poon, L., Sequelstra, A., Sethi, R., Zhang, R., Zieran, L. and Svirkas, R.R., Wan, K., Weinburg, Y., Zhang, R., Zieran, L. and Rubin, G.N. of *Drosophila melanogaster*

[illegible]

Rubin, G.M.
 Direct Submission
 Submitted (22-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Sep 3, 1999 this sequence version replaced g1:5670517.
 For further information about this sequence, including its location
 on chromosomes, please visit our sequence
 comment page at <http://www.ncbi.nlm.nih.gov/seq/seqcomment.cgi?seq=1000000000> and email
rubin@genomecenter.lbl.gov

and relationship to other sequences, and an archive Web site (<http://www.infinity.org/sequence/>) or accession to biggerruftp1.berkeley.edu. All contigs in this submission to biggerruftp1.berkeley.edu: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently follows the following order of the pieces

* consists of 99 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

979-contig of 979 bp in length

*	1	1059:	gap of unknown length
*	980	1059:	gap of 521 bp in length
*	1060	1059:	contig of unknown length
*	1561	1660:	gap of unknown length
*	1661	1660:	gap of 707 bp in length
*	2368	2447:	gap of unknown length
*	2448	2447:	gap of 872 bp in length
*	3319:	3319:	contig of unknown length
*	3320	3399:	gap of unknown length
*	3400	4062:	contig of 663 bp in length
*	4063	4143:	gap of unknown length
*	4143	5113:	contig of 971 bp in length
*	5114	5193:	gap of unknown length
*	5194	5741:	gap of 548 bp in length
*			contig of 548 bp in length

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 7; Length 2441;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cttggccttaccgtatccg 20
Db 764 cttggccttaccgtatccg 745

RESULT 4

LOCUS MAMAHNY1 9085 bp DNA
DEFINITION Mus musculus mahogany (mg) gene, exons.
ACCESSION AF120317
VERSION AF120317.1 GI:4545287
KEYWORDS
SEGMENT
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
TITLE
JOURNAL
Schlossman, S.F., Duke-Cohan, J.S. and Barsh, G.S.
The mouse mahogany locus encodes a transmembrane form of human attractin
Nature 398 (6723), 152-156 (1999)
JOURNAL MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
Schlossman, S.F., Duke-Cohan, J.S. and Barsh, G.S.
Direct submission
Submitted (14-JAN-1999) HMMI, Stanford, Beckman Center B271,
Stanford, CA 94305-5523, USA
FEATURES
Source
Location/Qualifiers
1..9085
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/clone="BAC 38989"
1870..1931
/gene="mg"
join(1870..1931,6879..6957)
/note="transmembrane-region site"
exon
6879..6957
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exon
BASE COUNT 2650 a 1817 c 1800 g 2818 t
ORIGIN

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 12; Length 9085;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cttggccttaccgtatccg 20
Db 6968 cttggccttaccgtatccg 6949

RESULT 5

LOCUS DMGLASS 9954 bp DNA
DEFINITION Drosophila glass gene encoding a zinc finger protein.
ACCESSION X15400
VERSION X15400.1 GI:8015
KEYWORDS
glass gene; transcription factor; zinc finger protein.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;

REFERENCE

AUTHORS
TITLE
JOURNAL
Moses, K.
Direct Submission
Submitted (19-JUL-1989) Moses K., Howard Hughes Medical Institute,
Department of Biochemistry, University of California, Room 539 LSA,
Berkeley California 94720
2 (bases 3949 to 4410; 5057 to 5193; 5482 to 5612; 6092 to 7584;
7981 to 9044)
Moses, K., Ellis, M.C. and Rubin, G.M.
The glass gene encodes a zinc-finger protein required by Drosophila
photoreceptor cells
Nature 340 (6234), 531-536 (1989)
89365138
COMMENT
The open reading frame in the cDNA seqs. derived from a different
wild-type strain differs at four positions from that of the genomic
seq:
Glu 60 is replaced by Gln, Pro 361 by Ser, Met 362 by Leu and Ser
377 by Thr (nucleotide changes are not specified in [2]).
Location/Qualifiers
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/clone="lib-Sau3a part. in lambda fix."
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4189..9021
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4193
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4411..5056
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SLEPSPGASINFAAGNPHOASLSYTYVPHOMLISBNHNGOMHSHOHOHOS
OYASHVNSLLQSGGNNIGNSAGVANAACVETSTAGTAAPPPEPAAAYPSK
SYNSMNTMHHGAGDAGVPMCCSONMTPEPNSNTSAAALAAAVNTLPPLLSG
HIPASVSTFADFRAPAPPGIGALPPTVGEKSPSPANSIAGIYPTVGNGQGT
PHEKPTSYOAAALGSLSEAEDEDSNEDIDGSGSGGEMKPTLCLGKTYAPSS
TLKTLRHSGERPIYRCPCNKSFSQANLTAHVRHTGQKFPKPCIDRFSQSSSV

FEATURES

source

gene

exon

precursor_RNA

misc_feature

misc_feature

intron

exon

CDS

File copy

25 18.4 92.0 2805 2 AF053963
26 18.4 92.0 2805 2 AF053968
27 18.4 92.0 2806 2 AF053968
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32 18.4 92.0 2806 2 AF053968
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34 18.4 92.0 2806 2 AF053968
35 18.4 92.0 2806 2 AF053968
36 18.4 92.0 2806 2 AF053968
37 18.4 92.0 2806 2 AF053968
38 18.4 92.0 2806 2 AF053968
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ALIGNMENTS

RESULT 1
A98413 20 bp DNA
LOCUS Sequence 2 from Patent WO912949.
ACCESSION A98413
VERSION A98413.1 GI:6781514
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gataagctggtgtgtaagc 20
DB 1 GATAGCTGGGTGTGTAAAC 20
RESULT 2
PARRN235 2893 bp DNA
LOCUS Pseudomonas aeruginosa gene for 23S ribosomal RNA.
ACCESSION Y00432
VERSION Y00432.1 GI:45420
KEYWORDS 23S ribosomal RNA; ribosomal DNA.
SOURCE Pseudomonas aeruginosa.
ORGANISM Pseudomonas aeruginosa.
REFERENCE 1 (bases 1 to 2893)
AUTHORS Ubrich,N.
TITLE Direct Submission

JOURNAL Submitted (24-AUG-1987) Ubrich N., Institut fuer Biochemie,
Fachbereich Chemie, Freie Universitaet Berlin, Otto-Hahn-Bau,
Theissallee 63, D-1000 Berlin 33 (Dahlem)
REFERENCE 2 (bases 1 to 2893)
AUTHORS Toschka,H.Y., Hopfl,P., Lucwig,W., Schleifer,K.H., Ubrich,N. and Erdmann,V.A.
TITLE Complete nucleotide sequence of a 23S ribosomal RNA gene from Pseudomonas aeruginosa
JOURNAL Nucleic Acids Res. 15 (17), 7182 (1987)
MEDLINE 88015558
FEATURES
source
Location/Qualifiers
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/organism="Pseudomonas aeruginosa"
/strain="ATCC 10145"
/db_xref="taxon:287"
/clone="pPA4.6"
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RNA
BASE COUNT 754 a 621 c 904 g 614 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gataagctggtgtgtaagc 20
DB 2823 GATAGCTGGGTGTGTAAAC 2842
RESULT 3
YE077925 2906 bp DNA
LOCUS Yersinia enterocolitica 23S ribosomal RNA (rrl) gene, complete
DEFINITION sequence.
ACCESSION Y077925
VERSION Y077925.1 GI:3335033
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN

Query Match 98.0%; Score 19.6; DB 2; Length 2906;
Best Local Similarity 95.0%; Pred. No. 5.3;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 gataagctggtgtgtaagc 20
RESULT 4
YE077925 2906 bp DNA
LOCUS Yersinia enterocolitica 23S ribosomal RNA (rrl) gene, complete
DEFINITION sequence.
ACCESSION Y077925
VERSION Y077925.1 GI:3335033
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN